

SEQUENCE LISTING



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<120> Thermostable Reverse Transcriptases and Uses Thereof

<130> 0942.5040001/RWE/MTT

<140> US 09/845,157

<141> 2001-05-01

<150> US 60/207,196

<151> 2000-05-26

<160> 6

<170> PatentIn version 3.0

<210> 1

<211> 2151

<212> DNA

<213> Moloney-Murine Leukemia Virus

<220>

<221> CDS

<222> (1)..(2151)

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Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys His

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atg acc cta aat ata gaa gat gag tat cgg cta cat gag acc tca aaa Met Thr Leu Asn Ile Glu Asp Glu Tyr Arg Leu His Glu Thr Ser Lys 35 40 45			144
gag cca gat gtt tct cta ggg tcc aca tgg ctg tct gat ttt cct cag Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln 50 55 60			192
gcc tgg gcg gaa acc ggg ggc atg gga ctg gca gtt cgc caa gct cct Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro 65 70 75 80			240
ctg atc ata ctt ctg aaa gca acc tct acc ccc gtg tcc ata aaa caa Leu Ile Ile Leu Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln 85 90 95			288
tac ccc atg tca caa gaa gcc aga ctg ggg atc aag ccc cac ata cag Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln 100 105 110			336
aga ctg ttg gac cag gga ata ctg gta ccc tgc cag tcc ccc tgg aac Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn 115 120 125			384
acg ccc ctg cta ccc gtc aag aaa ccc ggg act aat gat tac agg cct Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro 130 135 140			432
gtc caa gat ctg aga gag gtc aac aaa cgc gta gaa gac atc cac ccc Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro 145 150 155 160			480
acc gta ccc aac ccc tac aac ctc ttg agt ggg ctc cca ccg tcc cac Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His 165 170 175			528
cag tgg tac act gtt cta gac tta aaa gat gcc ttt ttc tgc ctg aga Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe Phe Cys Leu Arg 180 185 190			576
ctc cac ccg acg tct cag cct ctc ttc gcc ttt gaa tgg aga gac cca Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro 195 200 205			624
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ttc aaa aac agt ccc acc ctg ttt gat gag gca ctg cgc aga gac cta Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu Arg Arg Asp Leu 225 230 235 240			720
gca gac ttc cgg atc cag cac cca gac ttg atc ctg cta cag tac gta Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu Leu Gln Tyr Val 245 250 255			768
gat gac tta ctg ctg gcc gcc act tct gag ctc gac tgc caa caa ggt Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp Cys Gln Gln Gly 260 265 270			816

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Thr Arg Ala Leu Leu Gln Thr Leu Gly Asp Leu Gly Tyr Arg Ala Ser	
275 280 285	
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Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr	
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ctt cta aaa gag ggt cag aga tgg ctg act gag gcc aga aaa gag act	960
Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr	
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Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe	
325 330 335	
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Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu	
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Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly Thr Leu Phe Asn	
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tgg ggc cca gac caa caa aag gcc tat caa gaa atc aag caa gct ctt	1152
Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile Lys Gln Ala Leu	
370 375 380	
cta act gcc cca gcc ctg ggg ttg cca gat ttg act aag ccc ttt gaa	1200
Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu	
385 390 395 400	
ctc ttt gtc gac gag aag cag ggc tac gcc aaa ggt gtc cta acg caa	1248
Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln	
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aaa ctg gga cct tgg cgt cgg ccg gtg gcc tac ctg tcc aaa aag cta	1296
Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu	
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Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala	
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Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro	
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Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro	
465 470 475 480	
ccc gat cga tgg ctt tcc aac gcc cgg atg act cac tat cag gcc ttg	1488
Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu	
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ctt ttg gac acg gac cgg gtc cag ttc gga ccg gtg gta gcc ctg aac	1536
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Leu Asp Ile Leu Ala Glu Ala His Gly Thr Arg Pro Asp Leu Thr Asp	
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Gln Pro Leu Pro Asp Ala Asp His Thr Trp Tyr Thr Gly Gly Ser Ser	
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acc gag gta atc tgg gct aaa gcc ctg cca gcc ggg aca tcc gct cag	1776
Thr Glu Val Ile Trp Ala Lys Ala Leu Pro Ala Gly Thr Ser Ala Gln	
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cgg gct cag ctg ata gca ctc acc cag gcc cta agg atg gca gaa ggt	1824
Arg Ala Gln Leu Ile Ala Leu Thr Gln Ala Leu Arg Met Ala Glu Gly	
595 600 605	
aag aag cta aat gtt tat acg aat tcc cgt tat gct ttt gct act gcc	1872
Lys Lys Leu Asn Val Tyr Thr Asn Ser Arg Tyr Ala Phe Ala Thr Ala	
610 615 620	
cat atc cat gga gaa ata tac aga agg cgt ggg ttg ctc aca tca gaa	1920
His Ile His Gly Glu Ile Tyr Arg Arg Arg Gly Leu Leu Thr Ser Glu	
625 630 635 640	
ggc aaa gag atc aaa aat aag gac gag ata ttg gcc cta cta aaa gcc	1968
Gly Lys Glu Ile Lys Asn Lys Asp Glu Ile Leu Ala Leu Leu Lys Ala	
645 650 655	
ctc ttt ctg ccc aaa aga ctt agc ata atc cat tgt cca gga cat caa	2016
Leu Phe Leu Pro Lys Arg Leu Ser Ile Ile His Cys Pro Gly His Gln	
660 665 670	
aag gga cac agc gcc gag gct aga ggc aac cgg atg gct gac caa gcg	2064
Lys Gly His Ser Ala Glu Ala Arg Gly Asn Arg Met Ala Asp Gln Ala	
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gcc cga aag gca gcc atc aca gag aat cca gac acc tct acc ctc ctc	2112
Ala Arg Lys Ala Ala Ile Thr Glu Asn Pro Asp Thr Ser Thr Leu Leu	
690 695 700	
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<212> PRT

<213> Moloney-Murine Leukemia Virus

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Met	Thr	Leu	Asn	Ile	Glu	Asp	Glu	Tyr	Arg	Leu	His	Glu	Thr	Ser	Lys	
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Glu	Pro	Asp	Val	Ser	Leu	Gly	Ser	Thr	Trp	Leu	Ser	Asp	Phe	Pro	Gln	
	50					55					60					
Ala	Trp	Ala	Glu	Thr	Gly	Gly	Met	Gly	Leu	Ala	Val	Arg	Gln	Ala	Pro	
65					70				75						80	
Leu	Ile	Ile	Leu	Leu	Lys	Ala	Thr	Ser	Thr	Pro	Val	Ser	Ile	Lys	Gln	
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Tyr	Pro	Met	Ser	Gln	Glu	Ala	Arg	Leu	Gly	Ile	Lys	Pro	His	Ile	Gln	
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Arg	Leu	Leu	Asp	Gln	Gly	Ile	Leu	Val	Pro	Cys	Gln	Ser	Pro	Trp	Asn	
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Thr	Pro	Leu	Leu	Pro	Val	Lys	Lys	Pro	Gly	Thr	Asn	Asp	Tyr	Arg	Pro	
	130					135					140					
Val	Gln	Asp	Leu	Arg	Glu	Val	Asn	Lys	Arg	Val	Glu	Asp	Ile	His	Pro	
145					150					155					160	
Thr	Val	Pro	Asn	Pro	Tyr	Asn	Leu	Leu	Ser	Gly	Leu	Pro	Pro	Ser	His	
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Gln	Trp	Tyr	Thr	Val	Leu	Asp	Leu	Lys	Asp	Ala	Phe	Phe	Cys	Leu	Arg	
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Leu	His	Pro	Thr	Ser	Gln	Pro	Leu	Phe	Ala	Phe	Glu	Trp	Arg	Asp	Pro	
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Ala	Asp	Phe	Arg	Ile	Gln	His	Pro	Asp	Leu	Ile	Leu	Leu	Gln	Tyr	Val	
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Thr Arg Ala Leu Leu Gln Thr Leu Gly Asp Leu Gly Tyr Arg Ala Ser  
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Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr  
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Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr  
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Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe  
325 330 335

Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu  
340 345 350

Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly Thr Leu Phe Asn  
355 360 365

Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile Lys Gln Ala Leu  
370 375 380

Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu  
385 390 395 400

Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln  
405 410 415

Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu  
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Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala  
435 440 445

Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro  
450 455 460

Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro  
465 470 475 480

Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu  
485 490 495

Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn  
500 505 510

Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys  
515 520 525

Leu Asp Ile Leu Ala Glu Ala His Gly Thr Arg Pro Asp Leu Thr Asp  
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Gln Pro Leu Pro Asp Ala Asp His Thr Trp Tyr Thr Gly Gly Ser Ser  
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Leu Leu Gln Glu Gly Gln Arg Lys Ala Gly Ala Ala Val Thr Thr Glu  
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Thr Glu Val Ile Trp Ala Lys Ala Leu Pro Ala Gly Thr Ser Ala Gln  
580 585 590

Arg Ala Gln Leu Ile Ala Leu Thr Gln Ala Leu Arg Met Ala Glu Gly  
595 600 605

Lys Lys Leu Asn Val Tyr Thr Asn Ser Arg Tyr Ala Phe Ala Thr Ala  
610 615 620

His Ile His Gly Glu Ile Tyr Arg Arg Arg Gly Leu Leu Thr Ser Glu  
625 630 635 640

Gly Lys Glu Ile Lys Asn Lys Asp Glu Ile Leu Ala Leu Leu Lys Ala  
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Leu Phe Leu Pro Lys Arg Leu Ser Ile Ile His Cys Pro Gly His Gln  
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Lys Gly His Ser Ala Glu Ala Arg Gly Asn Arg Met Ala Asp Gln Ala  
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<213> Artificial

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18

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<213> Escherichia coli

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gctatgacca tgattacgcc aagcttgcac gcctgcaggt cgactctaga ggatccccgg 180

gtaccgagct cgaattcact ggccgtcggt ttacaacgtc gtgactggga aaaccctggc 240

gttaccacaac ttaatcgct tgcagacat ccccttttcg ccagctggcg taatagcg 298